us-09-924-102-2.rspt

OM protein - protein search, using sw model

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Run on:        May 29, 2003, 15:27:08 ; Search time 79 seconds
                                        (without alignments)
                                        211.263 Million cell updates/sec

Title:         US-09-924-102-2
Perfect score: 81
Sequence:      1 MLLSTHLFIYLFIYFLSYSL...........RWGGQGGRGGTADTGGMFLS 81
Scoring table:
               OLIGO
               Gapop 60.0 , Gapext 60.0
Searched:      671580 seqs, 20647115 residues
Word size :    0
Total number of hits satisfying chosen parameters:    671580
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries
Database :     SPTREMBL_21:*
               1: sp_archea:*
               2: sp_bacteria:*
               3: sp_fungi:*
               4: sp_human:*
               5: sp_invertebrate:*
               6: sp_mammal:*
               7: sp_mhc:*
               8: sp_organelle:*
               9: sp_phage:*
              10: sp_plant:*
              11: sp_rodent:*
              12: sp_virus:*
              13: sp_vertebrate:*
              14: sp_unclassified:*
              15: sp_rvirus:*
              16: sp_bacteriap:*
              17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 8 | 9.9 | 135 | 4 | Q8WYS0 | Q8wys0 homo sapien |
| 2 | 8 | 9.9 | 151 | 4 | Q96LU0 | Q96lu0 homo sapien |
| 3 | 8 | 9.9 | 381 | 5 | O76450 | O76450 strongyloce |
| 4 | 8 | 9.9 | 447 | 5 | Q9biv1 | Q9biv1 argiope aur |
| 5 | 8 | 9.9 | 450 | 4 | Q96C50 | Q96c50 homo sapien |
| 6 | 8 | 9.9 | 485 | 9 | O8SCI0 | O8sci0 propionibac |
| 7 | 8 | 9.9 | 900 | 11 | Q9EQK8 | Q9eqk8 mus musculu |
| 8 | 8 | 9.9 | 910 | 11 | Q9YC4 | Q9yc4 mus musculu |
| 9 | 8 | 9.9 | 941 | 11 | Q9TTA5 | Q9tta5 bos taurus |
| 10 | 7 | 9.9 | 19 | 11 | Q06028 | Q06028 mus musculu |
| 11 | 7 | 8.6 | 137 | 2 | Q9XCQ4 | Q9xcq4 haemophilus |
| 12 | 7 | 8.6 | 137 | 16 | Q92TF3 | Q92tf3 rhizobium m |
| 13 | 7 | 8.6 | 145 | 3 | Q9RRG3 | Q9rrg3 deinococcus |
| 14 | 7 | 8.6 | 175 | 11 | Q9D3N7 | Q9d3n7 mus musculu |
| 15 | 7 | 8.6 | 194 | 10 | Q9ZUR8 | Q9zur8 arabidopsis |
| 16 | 7 | 8.6 | 195 | 5 | O02126 | O02126 caenorhabdi |

| | | | | | |
|---|---|---|---|---|---|
| 17 | 7 | 8.6 | 214 | 16 | Q8UFT3 | Q8uft3 agrobacteri |
| 18 | 7 | 8.6 | 244 | 4 | Q9H700 | Q9h700 homo sapien |
| 19 | 7 | 8.6 | 267 | 11 | Q9DBX0 | Q9dbx0 mus musculu |
| 20 | 7 | 8.6 | 299 | 4 | Q96G00 | Q96g00 homo sapien |
| 21 | 7 | 8.6 | 304 | 3 | Q92194 | Q92194 aspergillus |
| 22 | 7 | 8.6 | 311 | 5 | Q96200 | Q96200 plasmodium |
| 23 | 7 | 8.6 | 313 | 8 | Q9MJQ2 | Q9mjq2 podospora c |
| 24 | 7 | 8.6 | 316 | 17 | Q82VK5 | Q82vk5 pyrobaculum |
| 25 | 7 | 8.6 | 322 | 17 | Q9HJ15 | Q9hj15 thermoplasm |
| 26 | 7 | 8.6 | 357 | 10 | Q9LVT8 | Q9lvt8 arabidopsis |
| 27 | 7 | 8.6 | 369 | 5 | Q9V5V7 | Q9v5v7 drosophila |
| 28 | 7 | 8.6 | 380 | 4 | Q9UFV7 | Q9ufv7 homo sapien |
| 29 | 7 | 8.6 | 381 | 16 | Q8XBS1 | Q8xbs1 escherichia |
| 30 | 7 | 8.6 | 453 | 13 | P87373 | P87373 gallus gall |
| 31 | 7 | 8.6 | 469 | 10 | Q888A7 | Q888a7 arabidopsis |
| 32 | 7 | 8.6 | 478 | 2 | P95758 | P95758 streptomyce |
| 33 | 7 | 8.6 | 504 | 10 | Q8VYJ6 | Q8vyj6 arabidopsis |
| 34 | 7 | 8.6 | 507 | 10 | Q9SKF3 | Q9skf3 arabidopsis |
| 35 | 7 | 8.6 | 519 | 12 | Q91MK3 | Q91mk3 menangle vi |
| 36 | 7 | 8.6 | 534 | 10 | O80853 | O80853 arabidopsis |
| 37 | 7 | 8.6 | 546 | 10 | O04031 | O04031 arabidopsis |
| 38 | 7 | 8.6 | 581 | 4 | O96822 | O96822 homo sapien |
| 39 | 7 | 8.6 | 581 | 4 | O14927 | O14927 homo sapien |
| 40 | 7 | 8.6 | 583 | 4 | Q9UJH4 | Q9ujh4 homo sapien |
| 41 | 7 | 8.6 | 606 | 16 | Q9WXN8 | Q9wxn8 thermotoga |
| 42 | 7 | 8.6 | 607 | 16 | Q83U2 | Q83u2 nicotiana b |
| 43 | 7 | 8.6 | 619 | 4 | Q9NXQ5 | Q9nxq5 homo sapien |
| 44 | 7 | 8.6 | 622 | 10 | Q9SKF2 | Q9skf2 arabidopsis |
| 45 | 7 | 8.6 | 628 | 10 | Q9XEM7 | Q9xem7 oryza satiy |

ALIGNMENTS

RESULT 1
Q8WYS0
ID      Q8WYS0          PRELIMINARY;    PRT;    135 AA.
AC      Q8WYS0;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      GLO13.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=LIVER;
RA      Liu F., Xu X.R., Qian B.Z., Xiao H., Chen Z., Han Z.;
RT      "A novel gene expressed in human liver non-tumor-tissue.";
RL      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF361491; AAL57216.1; -.
SQ      SEQUENCE   135 AA;  15273 MW;  49870F479A2662EA CRC64;

Query Match             9.9%;  Score 8;  DB 4;  Length 135;
Best Local Similarity   100.0%;  Pred. No. 0.9;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 SLGDRARL 26
              ||||||||
Db         40 SLGDRARL 47

RESULT 2
Q96LU0
ID      Q96LU0          PRELIMINARY;    PRT;    151 AA.
AC      Q96LU0;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      CDNA FLJ25069 fis, clone CBL05145.
OS      Homo sapiens (Human).

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CEREBELLUM;
RA   Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK057798; BAB71579.1; -.
SQ   SEQUENCE   151 AA;   16915 MW;   99A24D0C477DBF36 CRC64;

Qy   19 SLGDRARL 26
        ||||||||
Db   48 SLGDRARL 55

Query Match             9.9%;
Best Local Similarity   100.0%;           Pred. No. 0.99;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
                                          Score 8;  DB 4;  Length 151;

RESULT 3
076450
ID   076450         PRELIMINARY;    PRT;   381 AA.
AC   076450;
DT   01-NOV-1998 (TREMBLrel. 08, Created)
DT   01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT   01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE   Spicule matrix protein precursor.
GN   SM37.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotida;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lee Y.-H., Britten R.J., Davidson E.H.;
RT   "SM37, a new skeletogenic gene of the sea urchin embryo isolated by
RT   regulatory target site screening.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF067737; AAC33762.1; -.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; lectin_c; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Matrix protein; Signal.
FT   SIGNAL        1     16
FT   CHAIN        17    381
SQ   SEQUENCE   381 AA;   39136 MW;   62F9320A59BD91F4 CRC64;

Qy   64 GGQGGRGG 71
        ||||||||
Db  235 GGQGGRGG 242

Query Match             9.9%;
Best Local Similarity   100.0%;           Pred. No. 2.3;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
                                          Score 8;  DB 5;  Length 381;

RESULT 4
Q9BIV1
ID   Q9BIV1         PRELIMINARY;    PRT;   447 AA.
AC   Q9BIV1;
DT   01-JUN-2001 (TREMBLrel. 17, Created)
DT   01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE   Major ampullate spidroin 1 (Fragment).
GN   MASP1.
OS   Argiope aurantia.
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Araneoidea; Araneidae; Argiope.
OX   NCBI_TaxID=156844;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21179804; PubMed=11283372;
RA   Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.;
RT   "Extreme Diversity, Conservation, and Convergence of Spider Silk
RT   Fibroin Sequences.";
RL   Science 291:2603-2605(2001).
DR   EMBL; AF352262; AAK30591.1; -.
DR   InterPro; IPR000817; Prion.
DR   PRINTS; PR00341; PRION.
FT   NON_TER       1      1
FT   NON_TER     447    447
SQ   SEQUENCE   447 AA;   35630 MW;   78D160B7E6DF24C7 CRC64;

Qy   64 GGQGGRGG 71
        ||||||||
Db  171 GGQGGRGG 178

Query Match             9.9%;
Best Local Similarity   100.0%;           Pred. No. 2.6;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
                                          Score 8;  DB 5;  Length 447;

RESULT 5
Q96C50
ID   Q96C50         PRELIMINARY;    PRT;   450 AA.
AC   Q96C50;
DT   01-DEC-2001 (TREMBLrel. 19, Created)
DT   01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE   Hypothetical 47.4 kDa protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014678; AAH14678.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   450 AA;   47417 MW;   93CEE7B44D2C1FB6 CRC64;

Qy   23 RARLCLRK 30
        ||||||||
Db  438 RARLCLRK 445

Query Match             9.9%;
Best Local Similarity   100.0%;           Pred. No. 2.7;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
                                          Score 8;  DB 4;  Length 450;

RESULT 6
Q8SCI0
ID   Q8SCI0         PRELIMINARY;    PRT;   485 AA.
AC   Q8SCI0;
DT   01-JUN-2002 (TREMBLrel. 21, Created)
DT   01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE   Orf6.
OS   Propionibacterium phage phiB5.
OC   Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX   NCBI_TaxID=189836;
RN   [1]

RP   SEQUENCE FROM N.A.
RX   MEDLINE=21886396; PubMed=11889111;
RA   Chopin M.C., Rouault A., Ehrlich S.D., Gautier M.;
RP   SEQUENCE FROM N.A.
RX   "Filamentous Phage Active on the Gram-Positive Bacterium
RA   Propionibacterium freudenreichii.";
RL   J. Bacteriol. 184:2030-2033(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chopin M.C., Rouault A., Gautier M.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF42860; AAL91699.1; -.
SQ   SEQUENCE   485 AA;  48825 MW;  0B4F44ABE3DE91A4 CRC64;

Qy          64 GGQGGRGG 71
                |||||||||
Db         363 GGQGGRGG 370

Query Match             9.9%;  Score 8;  DB 9;  Length 485;
Best Local Similarity   100.0%;  Pred. No. 2.8;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 7
ID   Q9EQK8
AC   Q9EQK8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HepA-related protein HARP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20313894; PubMed=10857751;
RA   Coleman M.A., Eisen J.A., Mohrenweiser H.W.;
RT   "Cloning and characterization of HARP/SMARCAL1: a prokaryotic HepA-
RT   related SNF2 helicase protein from human and mouse.";
RL   Genomics 65:274-282(2000).
EMBL; AF209773; AAG47648.1; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   Pfam; PF00270; SNF2_N; 1.
DR   Pfam; PF00176; SNF2_N; 1.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
KW   ATP-binding; Helicase.
SQ   SEQUENCE   900 AA;  99768 MW;  E89E43783FD4B16F CRC64;

Qy          30 KTKQQOKE 37
                |||||||||
Db         647 KTKQQOKE 654

Query Match             9.9%;  Score 8;  DB 11;  Length 900;
Best Local Similarity   100.0%;  Pred. No. 5;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20313894; PubMed=10857751;
RA   Coleman M.A., Eisen J.A., Mohrenweiser H.W.;
RT   "Cloning and characterization of HARP/SMARCAL1: a prokaryotic HepA-
RT   related SNF2 helicase protein from human and mouse.";
RL   Genomics 65:274-282(2000).
DR   EMBL; AF088884; AAF24985.1; -.
DR   MGD; MGI:1859183; Smarcal1.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR000330; SNF2_N.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00176; SNF2_N; 1.
DR   SMART; SM00490; HELICc; 1.
KW   ATP-binding; Helicase.
SQ   SEQUENCE   910 AA;  101042 MW;  3F69C87A1BE5D8C5 CRC64;

Qy          30 KTKQQOKE 37
                |||||||||
Db         647 KTKQQOKE 654

Query Match             9.9%;  Score 8;  DB 11;  Length 910;
Best Local Similarity   100.0%;  Pred. No. 5;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 8
ID   Q9QYC4
AC   Q9QYC4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HepA-related protein Harp.
GN   SMARCAL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RESULT 9
ID   Q9TTA5
AC   Q9TTA5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DNA-dependent ATPase A.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=THYMUS;
RX   MEDLINE=20179861; PubMed=10713074;
RA   Muthuswami R., Truman P.A., Mesner L.D., Hockensmith J.W.;
RT   "A Eukaryotic SW12/SNF2 Domain, an Exquisite Detector of Double-
RT   stranded to Single-stranded DNA Transition Elements.";
RL   J. Biol. Chem. 275:7648-7655(2000).
DR   EMBL; AF173643; AAF22285.1; -.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR000330; SNF2_N.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00176; SNF2_N; 1.
DR   SMART; SM00490; HELICc; 1.
KW   ATP-binding; Helicase.
SQ   SEQUENCE   941 AA;  104915 MW;  AC3309EF813E931B CRC64;

Qy          30 KTKQQOKE 37
                |||||||||
Db         647 KTKQQOKE 654

Query Match             9.9%;  Score 8;  DB 6;  Length 941;
Best Local Similarity   100.0%;  Pred. No. 5.2;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 10
ID   Q06028
AC   Q06028;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Qy          30 KTKQQOKE 37
                |||||||||
Db         686 KTKQQOKE 693

```
DE   Sqa-2 antigen (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91065311; PubMed=2249652;
RA   Ulker N., Lewis K.D., Hood L.E., Stroynowski I.;
RT   "Activated T cells transcribe an alternatively spliced mRNA encoding a
RT   soluble form of Qa-2 antigen.";
RL   EMBO J. 9:3839-3847(1990).
DR   EMBL; X57330; CAA40607.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   19 AA;   1956 MW;  F2EA894D75527770 CRC64;

Qy           62  RWGGQGG  68
                 |||||||
Db            6  RWGGQGG  12

RESULT 11
Q9XCQ4
ID   Q9XCQ4              PRELIMINARY;       PRT;   137 AA.
AC   Q9XCQ4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Hypothetical 15.9 kDa protein.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.M., Janson H.;
RC   STRAIN=HK695;
RT   "Different organization and regulation of the glpTQ operons between
RT   type b and nontypeable Haemophilus influenzae.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF132900; AAD38341.1; -.
DR   InterPro; IPR000620; DUF6.
DR   Pfam; PF00892; DUF6; 1.
KW   Hypothetical protein.
SQ   SEQUENCE  137 AA;   15901 MW;  D9678F2624C7891C CRC64;

Query Match             8.6%;  Score 7;  DB 11;  Length 137;
Best Local Similarity   100.0%;  Pred. No. 1.9;
Matches    7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy            7  LFIYLFI  13
                 |||||||
Db           71  LFIYLFI  77

RESULT 12
Q92TF3
ID   Q92TF3              PRELIMINARY;       PRT;   137 AA.
AC   Q92TF3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative plasmid stability protein.
GN   RB1571 OR SMB21651.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OG   Plasmid pSymB (megaplasmid 2).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;

RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396508; PubMed=11481431;
RA   Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA   Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA   Golding B., Puehler A.;
RT   "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT   fixing endosymbiont Sinorhizobium meliloti.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR   EMBL; AL603647; CAC49970.1; -.
DR   InterPro; IPR002716; PIN.
DR   Pfam; PF01850; PIN; 1.
KW   Plasmid; Hypothetical protein; Complete proteome.
SQ   SEQUENCE  137 AA;   15059 MW;  77E4E5889F1734CFD CRC64;

Query Match             8.6%;  Score 7;  DB 16;  Length 137;
Best Local Similarity   100.0%;  Pred. No. 11;
Matches    7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy           50  SETLRKT  56
                 |||||||
Db           10  SETLRKT  16

RESULT 13
Q9RRG3
ID   Q9RRG3              PRELIMINARY;       PRT;   145 AA.
AC   Q9RRG3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein DR2529.
GN   DR2529.
OS   Deinococcus radiodurans.
OC   Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1;
RX   MEDLINE=20036896; PubMed=10567266;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
DR   EMBL; AE002082; AAF12073.1; -.
DR   TIGR; DR2529; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE  145 AA;   13709 MW;  4F295F5A23E1B4C8 CRC64;

Query Match             8.6%;  Score 7;  DB 16;  Length 145;
Best Local Similarity   100.0%;  Pred. No. 12;
Matches    7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy           67  GGRGGTA  73
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Db          128  GGRGGTA  134

RESULT 14
Q9D3N7
ID   Q9D3N7              PRELIMINARY;       PRT;   175 AA.
AC   Q9D3N7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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DE   5430401F13R1k protein.
GN   5430401F13R1K.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=HEAD;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   MGD; MGI:1918642; 5430401F13R1k.
DR   EMBL; AK017253; BAB30654.1; -.
SQ   SEQUENCE   175 AA;  18978 MW;  7DE4B9DAE66AF4F CRC64;

Qy         64 GGQGGRG 70
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Db        107 GGQGGRG 113
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RESULT 15
ID   Q9ZUR8       PRELIMINARY;     PRT;   194 AA.
AC   Q9ZUR8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   At2g37490 protein.
GN   At2g37490.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005896; AAC98065.1; -.
SQ   SEQUENCE   194 AA;  21116 MW;  82485F905192F741 CRC64;

Qy         54 RKTGKKG 60
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Db        146 RKTGKKG 152
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Query Match             8.6%;  Score 7;  DB 10;  Length 194;
Best Local Similarity  100.0%;           Pred. No. 16;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Search completed: May 29, 2003, 15:32:37
Job time : 82 secs